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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/720,178	11/25/2003	Tsunehiko Watanabe	HIRA.0131	4338

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EXAMINER	
LE, MIRANDA	

ART UNIT	PAPER NUMBER
2167	

DATE MAILED: 07/10/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/720,178	WATANABE ET AL.	
	Examiner	Art Unit	
	Miranda Le	2167	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 November 2003*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-7* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-7* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *08/18/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Information Disclosure Statement

1. Applicants' Information Disclosure Statement, filed 08/18/05, has been received, entered into the record, and considered. See attached form PTO-1449.

Drawings

2. The drawings are objected to because they fail to show necessary textual labels of features or symbols in Fig. 16 as described in the specification. For example, placing a label, "database", with elements 64, would give the viewer necessary detail to fully understand this element at a glance. A ***descriptive*** textual label for ***numbered elements*** 61, 62, 63 in this figure would be needed to fully and better understand these figures without substantial analysis of the detailed specification. Any structural detail that is of sufficient importance to be described should be shown in the drawing. Optionally, applicant may wish to include a table next to the present figure to fulfill this requirement. See 37 CFR 1.83. 37 CFR 1.84(n)(o) is recited below:

"(n) Symbols. Graphical drawing symbols may be used for conventional elements when appropriate. The elements for which such symbols and labeled representations are used must be adequately identified in the specification. Known devices should be illustrated by symbols which have a universally recognized conventional meaning and are generally accepted in the art. Other symbols which are not universally recognized may be used, subject to approval by the Office, if they are not likely to be confused with existing conventional symbols, and if they are readily identifiable.

(o) Legends. Suitable descriptive legends may be used, or may be required by the Examiner, where necessary for understanding of the drawing, subject to approval by the Office. They should contain as few words as possible."

Claim Rejections - 35 USC § 102

3. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless:
>
> (e) the invention was described in
>
> (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or
>
> (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

4. Claims 4-7 are rejected under 35 U.S.C. 102(e) as being anticipated by Yang et al. (US Pub. No. 2003/0100996).

Yang anticipated independent claims 4-7 by the following:

As per claim 4, Yang teaches a data search method comprising the steps of:

preparing index data (i.e. pathway IDs, [0062]) that is a collection of information indicating links between data in two databases, based on a plurality of databases (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt, UniGenea, public databases, [0054, 0062, 0063, 0064]) in which information about biological substances is stored ([0078 to 0082]);

preparing a table (i.e. Pathway table in Fig. 2, [0057]) defining the order of the links between the plurality of databases (i.e. Beginning with the first protein in the pathway, the most likely candidate for the second protein is chosen using the highest correlation coefficient with a value closest to one, [0079]) ([0078 to 0082]);

receiving a start database name (i.e. one species, [0075]), a target database name (i.e. target species, [0075]), and a data ID in the start database (i.e. the first protein, [0079]), which together constitute a search key ([0078 to 0082]);

acquiring a corresponding data ID in the target database by following those links (i.e. pathways, [0075]) among the links between data that match the order of the links between the databases (i.e. highest correlation coefficient, user-specified threshold, [0079]), while using as a start point the data ID in the start database that has been received (i.e. Beginning with the first protein in the pathway, [0079]), ([0078 to 0086]); and

displaying (i.e. display the screen in Fig. 4) the acquired data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0086]).

As per claim 5, Yang teaches a data search method comprising the steps of:

preparing index data (i.e. pathway IDs, [0062]) that is a collection of information indicating links between two databases and sequence data (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt, UniGenea, public databases, [0054, 0062, 0063, 0064]) for homology search, based on a plurality of databases in which information about biological substances is stored ([0078 to 0082]);

preparing a table (i.e. Pathway table in Fig. 2, [0057]) defining the order of the links between the plurality of databases (i.e. Beginning with the first protein in the pathway, the most likely candidate for the second protein is chosen using the highest correlation coefficient with a value closest to one, [0079]), ([0078 to 0082]);

receiving a start database name (i.e. one species, [0075]), a target database name (i.e. target species, [0075]), and input sequence data (i.e. information from sequence identity, [0080]), which together constitute a search key ([0078 to 0082]);

conducting a homology search for homology-search sequence data in the start database, using the input sequence data (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0086]);

acquiring a data ID of the target database by following those links among the links (i.e. pathways, [0075]) between data that match the order (i.e. highest correlation coefficient, user-specified threshold, [0079]) of the links between the plurality of databases, using as a start point the data ID in the start database that has been acquired by the homology search (i.e. Beginning with the first protein in the pathway, [0079]), ([0078 to 0086]); and

displaying (i.e. display the screen in Fig. 4) the acquired data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0086]).

As per claim 6, Yang teaches a data search system comprising:

index data (i.e. pathway IDs, [0062]) that is a collection of information indication links between data in two databases that is gathered from a plurality of databases (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt, UniGenea, public databases, [0054, 0062, 0063, 0064]) in which information about biological substances is stored ([0078 to 0082]);

a table (i.e. Pathway table in Fig. 2, [0057]) defining the order of the links between the plurality of databases (i.e. Beginning with the first protein in the pathway, the most likely

candidate for the second protein is chosen using the highest correlation coefficient with a value closest to one, [0079]) ([0078 to 0082]);

an input portion (i.e. submitting a query pathway and protein sequences, [0012]) for receiving a start database name (i.e. one species, [0075]), a target database name (i.e. target species, [0075]), and a data ID in the start database (i.e. the first protein, [0079]), which together constitute a search key (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0082]);

a search portion for acquiring a corresponding data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]) by following those links among the links between data that match the order (i.e. highest correlation coefficient, user-specified threshold, [0079]) of the links between the databases, while using as a start point the data ID in the start database that has been received (i.e. Beginning with the first protein in the pathway, [0079]), ([0078 to 0086]); and

displaying portion for displaying (i.e. display the screen in Fig. 4) the acquired data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0086]).

As per claim 7, Yang teaches a data search system comprising:

index data (i.e. pathway IDs, [0062]) that is a collection of sequence data for homology search and information indication links between data in two databases that is gathered from a plurality of databases (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt,

UniGenea, public databases, [0054, 0062, 0063, 0064]) in which information about biological substances is stored;

a table (i.e. Pathway table in Fig. 2, [0057]) defining the order of the links between the plurality of databases (i.e. Beginning with the first protein in the pathway, the most likely candidate for the second protein is chosen using the highest correlation coefficient with a value closest to one, [0079]), ([0078 to 0082]);

an input portion (i.e. submitting a query pathway and protein sequences, [0012]) for receiving a start database name (i.e. one species, [0075]), a target database name (i.e. target species, [0075]), and input sequence data (i.e. protein sequences, [0012]), which together constitute a search key (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0082]);

a first search portion for conducting a homology search for homology-search sequence data in the start database (i.e. the first protein in the pathway, [0079]), using the input sequence data (i.e. the proteins, he components need to be linked together, [0069]), ([0078 to 0082]);

a second search portion for acquiring a corresponding data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]) by following those links among the links between data that match the order (i.e. highest correlation coefficient, user-specified threshold, [0079]) of the links between the plurality of databases (i.e. the most likely candidate for the second protein is chosen using the highest correlation coefficient with a value closest to one, [0079]), using as a start point the data ID in the start database that has been acquired by homology search (i.e. Beginning with the first protein in the pathway, [0079]), ([0078 to 0086]); and

displaying portion for displaying (i.e. display the screen in Fig. 4) the acquired data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0086]).

Claim Rejections - 35 USC § 103

5. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

6. Claims 1-3 are rejected under 35 U.S.C. 103(a) as being unpatentable over Yang et al. (US Pub. No. 2003/0100996), in view of Wilbanks et al. (US Pub. No. 20020194201).

As per claim 1, Yang teaches a data distribution method comprising the steps of:

a plurality of databases (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt, UniGenea, public databases, [0054, 0062, 0063, 0064]) in which information about biological substances is stored ([0069]);

extracting data information indicating a link between data in two databases (i.e. pathway, [0062]), a detailed description of each data (i.e. expression data, [0062]), and sequence data for

homology search (i.e. information from sequence identity, [0080]), which together constitute an index (i.e. pathway IDs, [0062]); and

distributing the thus extracting index (i.e. pathway IDs, [0062]) ([0078 to 0082]).

Yang does not specifically teach downloading data from a plurality of databases.

Wilbanks teaches the step of downloading data form a plurality of databases (i.e. a priori knowledge of the semantics of the ontology that is represented by the associated biological/chemical databases 304 is built into the loader 302 of that ontology's external data files, [0069]).

Wilbanks also teaches the link between two databases (i.e. at least two of the related entities that are identified are linked, to thereby create an entity-relationship model that integrates the plurality of biological/chemical databases, Abstract).

It would have been obvious to one of ordinary skill of the art having the teachings of Yang and Wilbanks at the time the invention was made to modify the method of Yang to include downloading data from a plurality of databases, as taught by Wilbanks. One of ordinary skill in the art would be motivated to make this combination in order to represent an ontology and the entity-relationship model that integrates the plurality of biological/chemical databases creates an ontology network in view of Wilbanks, as doing so would give the added benefit of easily searching across multiple databases simultaneously as taught by Willbanks ([0007]).

As per claim 2, Yang teaches a data search method comprising the steps of:

a plurality of databases (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt, UniGenea, public databases, [0054, 0062, 0063, 0064]) in which information about biological substances is stored ([0069]);

extracting data information indicating links between data in two databases (i.e. pathway IDs, [0062]) ([0078 to 0082]);

receiving a start database name (i.e. one species, [0075]), a target database name (i.e. target species, [0075]), and a data ID in the start database (i.e. the first protein, [0079]), which together constitute a search key ([0078 to 0082]);

acquiring a data ID of the target database (i.e. the identity of each protein in the target species, [0075]) by following those links among the extracted links (i.e. pathways, [0075]) between data that match the predetermined order (i.e. highest correlation coefficient, user-specified threshold, [0079]) of a link between a plurality of databases, while referring to information indicating the predetermined order (i.e. sort hits by overall score in Fig. 4) of the link between the databases and using the received data ID in the start database as a start point (i.e. Beginning with the first protein in the pathway, [0079]) ([0078 to 0086]); and

displaying (i.e. display the screen in Fig. 4) the thus acquired data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]) ([0078 to 0086]).

Yang does not explicitly teach downloading data from a plurality of databases.

Wilbanks teaches the step of downloading data form a plurality of databases (i.e. a priori knowledge of the semantics of the ontology that is represented by the associated

biological/chemical databases 304 is built into the loader 302 of that ontology's external data files, [0069]).

Wilbanks also teaches the link between two databases (i.e. at least two of the related entities that are identified are linked, to thereby create an entity-relationship model that integrates the plurality of biological/chemical databases, Abstract).

It would have been obvious to one of ordinary skill of the art having the teachings of Yang and Wilbanks at the time the invention was made to modify the method of Yang to include downloading data from a plurality of databases as taught by Wilbanks. One of ordinary skill in the art would be motivated to make this combination in order to represent an ontology and the entity-relationship model that integrates the plurality of biological/chemical databases creates an ontology network in view of Wilbanks, as doing so would give the added benefit of easily searching across multiple databases simultaneously as taught by Willbanks ([0007]).

As per claim 3, Yang teaches a data search method comprising the steps of:

a plurality of databases (i.e. Pathways Database, a Uni-Protein Sequence Database, SwissProt, UniGenea, public databases, [0054, 0062, 0063, 0064]) in which information about biological substances is stored ([0069]);

extracting data information indicating link betweens data in two databases (i.e. pathway IDs, [0062]) and sequence data for homology search (i.e. information from sequence identity, [0080]) ([0078 to 0082]); and

receiving a start database name (i.e. one species, [0075]), a target database name (i.e. target species, [0075]), and input sequence data (i.e. submitting a query pathway and protein sequences, [0012]), which together constitute a search key ([0078 to 0082]);

conducting a homology search for homology-search sequence data in the start database, using the input sequence data (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]) ([0078 to 0082]);

acquiring a corresponding data ID of the target database by following those links among the extracted links (i.e. pathways, [0075]) between data that match the predetermined order (i.e. highest correlation coefficient, user-specified threshold, [0079]) of a link between databases, while referring to information indicating the predetermined order (i.e. sort hits by overall score in Fig. 4) of the link between the databases and using as a start point the data ID in the start database that has been acquired by the homology search (i.e. Beginning with the first protein in the pathway, [0079]) ([0078 to 0086]); and

displaying (i.e. display the screen in Fig. 4) the thus acquired data ID of the target database (i.e. the identity of each protein in the target species is determined by a sequence search against all protein sequences in the database, [0075]), ([0078 to 0086]).

Yang does not expressly teach downloading data from a plurality of databases.

Wilbanks teaches the step of downloading data form a plurality of databases (i.e. a priori knowledge of the semantics of the ontology that is represented by the associated biological/chemical databases 304 is built into the loader 302 of that ontology's external data files, [0069]).

Wilbanks also teaches the link between two databases (i.e. at least two of the related entities that are identified are linked, to thereby create an entity-relationship model that integrates the plurality of biological/chemical databases).

It would have been obvious to one of ordinary skill of the art having the teachings of Yang and Wilbanks at the time the invention was made to modify the method of Yang to include downloading data from a plurality of databases as taught by Wilbanks. One of ordinary skill in the art would be motivated to make this combination in order to represent an ontology and the entity-relationship model that integrates the plurality of biological/chemical databases creates an ontology network in view of Wilbanks, as doing so would give the added benefit of easily searching across multiple databases simultaneously as taught by Willbanks ([0007]).

Conclusion

7. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Miranda Le whose telephone number is (571) 272-4112. The examiner can normally be reached on Monday through Friday from 8:30 AM to 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John R. Cottingham, can be reached on (571) 272-7079. The fax number to this Art Unit is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 305-3900.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Miranda Le
June 14, 2006

GRETA ROBINSON
PRIMARY EXAMINER